
 224

(TM)

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MPorch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Apr 12 08:04:32 2000; User: time 13.26 Seconds

Tabular output not generated.

Title: >US-09-276-268-20

Description: (1-317) from US09276268. pep

Perfect Score: 2378

Sequence: 1 MFSSALPLMLGALVTVYS.....KKAAGKGVTSQAQAK 317

Scoring table: PAM 150

Gap 11

Searched: 188963 seqs, 23666106 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: 1-geneeq35

Statistics: Mean 33.327; Variance 130.318; scale 0.256

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	ID	Description	Pred. No.
2	1776	33.5	319	1	R27600	Human follistatin-3 pr	6.1e-155
3	789	33.2	317	1	R31396	Human follistatin (hfs	6.8e-70
4	785	33.0	304	1	R20062	Rat bcr-binding protein	1.82e-69
5	778	32.7	304	1	R20063	Human bcr-binding prot	2.99e-69
6	710	32.1	462	1	R07624	Human polypeptide chain	2.54e-40
7	506	31.3	462	1	R12377	Elongation factor-1a3	6.65e-40
8	428	31.0	460	1	R05567	Prostate tumor induc	7.40e-39
9	428	31.0	460	1	R05567	Prostate tumor induc	7.40e-39
10	428	31.0	460	1	R05567	Prostate tumor induc	7.40e-39
11	393	16.5	293	1	R05567	Plant elongation facto	3.59e-28
12	393	16.5	293	1	R05567	Plant elongation facto	3.59e-28
13	393	16.5	293	1	R05567	Plant elongation facto	3.59e-28
14	388	16.3	294	1	R05567	Plant elongation facto	3.59e-28
15	388	16.3	294	1	R05567	Plant elongation facto	3.59e-28
16	388	16.3	294	1	R05567	Plant elongation facto	3.59e-28
17	388	16.3	294	1	R05567	Plant elongation facto	3.59e-28
18	188	7.9	664	1	R03299	Human bcr-binding prot	1.17e-27
19	170	7.1	308	1	R17860	Human bcr-binding prot	8.9e-08
20	160	6.7	499	1	R07406	Follistatin related pr	4.28e-06
21	160	6.7	499	1	R07406	Follistatin related pr	4.28e-06
22	143	6.0	373	1	R05166	Transforming growth fa	6.55e-06
23	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
24	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
25	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
26	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
27	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
28	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
29	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
30	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
31	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
32	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
33	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
34	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
35	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
36	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
37	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
38	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
39	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
40	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
41	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
42	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
43	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
44	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06
45	140	5.9	304	1	R05166	Transforming growth fa	6.55e-06

24 140 5.9 374 1 W37497 Human TBP-2. 2.23e-03
 25 133 5.6 250 1 W34456 Human delta-2 protein 9.20e-03
 26 133 5.6 250 1 W34456 Human delta-2 protein 9.20e-03
 27 133 5.6 685 1 W34507 Human delta-2 protein. 9.20e-03
 28 133 5.6 685 1 W34507 Human delta-2 protein. 9.20e-03
 29 129 5.4 44 1 W04328 Human p-8 auto-antigen, rel 2.05e-02
 30 129 5.4 44 1 W04328 Human p-8 auto-antigen, rel 2.05e-02
 31 125 5.3 51 1 W04330 Human p-8 antigen ap1. 4.54e-02
 32 127 5.3 86 1 W02074 Human tumor associate 3.05e-02
 33 127 5.3 86 1 W02074 Human p80 type prot 3.05e-02
 34 122 5.1 104 1 R32608 Human p80 type prot 3.05e-02
 35 118 5.0 282 1 R79101 Prostaglandin I2 [PGI2 1.79e-01
 36 118 5.0 282 1 R79102 Prostaglandin I2 [PGI2 1.79e-01
 37 118 5.0 282 1 R79102 Prostaglandin I2 [PGI2 1.79e-01
 38 118 5.0 548 1 R37741 Xingmodulin/tumor de 1.78e-01
 39 110 4.5 436 1 W47222 Human secreted protein 1.78e-01
 40 108 4.5 1873 1 R44735 apo-E lipoprotein rece 1.78e-01
 41 108 4.5 1873 1 R44735 apo-E lipoprotein rece 1.78e-01
 42 108 4.5 1873 1 R44735 apo-E lipoprotein rece 1.78e-01
 43 105 4.4 612 1 W39256 Human partial mature m 2.15e-00
 44 105 4.4 846 1 R74692 Rat very low density 2.15e-00
 45 105 4.4 1351 1 R79475 Mouse lTRP-3. 2.15e-00

ALIGNMENTS

RESULT 1
 ID Y01098 standard; Protein; 263 AA.
 DC Y01098-1999 (first entry)
 DE Human follistatin-3 protein sequence.
 KW Follistatin-3; human; cancer; cellular differentiation disorder; reproductive system disorder; liver cirrhosis;
 KW osteosarcoma; idiopathic pulmonary fibrosis; pulmonary fibrosis; hepatoma;
 KW fibrotic disorder; osteoarthritis; hematopoiesis; infectious disease;
 KW hepatocellular carcinoma; cancer; silicosis; sarcoidosis; endotoxic shock; therapy.
 OS Homo sapiens
 PN M09510364-A1.
 PD 04-MAR-1999. 019710
 PR 25-AUG-1997; US-056248.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Duan R, Rubin SM;
 DR NPSDB: 228124/17.
 PT New follistatin-3 polypeptides and nucleic acids - used to develop products for treating e.g. cancers, male sterility, wound healing, infectious diseases, angiogenesis and autoimmune, inflammatory and other diseases.
 PS Claim 18: Fig 1: 109pp; English.
 CC This sequence is the follistatin-3 (FS3) protein of the invention.
 CC Differentiation disorders are a class of cancer and other cellular growth and differentiation disorders in which the normal cellular growth and differentiation system, FS3, can be used or to treat male sterility, FS3 may also be used to inhibit the activin-induced differentiation of follicular granulosa cell activity and as a result, induce the normal cellular growth and differentiation of the ovary. FS3 may also be used to inhibit the progression of gonadotroph adenomas, osteoarthritis, hepatomas, and other disorders including liver cirrhosis, osteoarthritis, and other fibrotic disorders. It may also be used to regulate hematopoiesis, and to treat osteoporosis. Antagonists of FS3 may be used to treat a deficiency in FS3, such as in the production of spermatozoa, to modulate gonadal and androgen biosynthesis, FS3 antagonists may also be used to treat infectious diseases including the activation of eosinophilic granulomatous disease, idiopathic pulmonary fibrosis by altering the activation of eosinophilic granulomatous disease, and the activation of eosinophilic granulomatous disease by preventing eosinophil production and activation. Endotoxic shock may also be treated by FS3 antagonists by inhibiting the activation of macrophages.
 SEQUENCE 263 AA.

Query Match 66.2% Score 1575; DB 1; Length 263;
Best Local Similarity 79.4%; Pred. No. 6,156-159; Matches 20; Conservative 27; Mismatches 23; Indels 3; Gaps 3;

Db 6 PGPALPMPALANALAVPSS-HSCGAPGVLGQGGQGGATGVLQVTPYAPKAS 64
Qy 3 SGLPPLPMPALVTVSSVGVKSSVGGVCGVQGGQGGATGVLQVTPYAPKAS 64
Qy 3 SGLPPLPMPALVTVSSVGVKSSVGGVCGVQGGQGGATGVLQVTPYAPKAS 64
Db 65 GNIDTANLTHPQNKLGTLGLVCLPKSCSDVCGPGACRAGKAGVPP-GRQ 123
Qy 65 GNIDTANLTHPQNKLGTLGLVCLPKSCSDVCGPGACRAGKAGVPP-GRQ 123
Qy 65 GNIDTANLTHPQNKLGTLGLVCLPKSCSDVCGPGACRAGKAGVPP-GRQ 123
Db 124 DCSGLPAPLVCGSSDQTLRDCTELVACRGHGPPLVSVVCGSCGPGACRAGKAGVPP-GRQ 123
Qy 124 DCSGLPAPLVCGSSDQTLRDCTELVACRGHGPPLVSVVCGSCGPGACRAGKAGVPP-GRQ 123
Qy 124 DCSGLPAPLVCGSSDQTLRDCTELVACRGHGPPLVSVVCGSCGPGACRAGKAGVPP-GRQ 123
Qy 123 NCGPAPGVLGSSDQTLRDCTELVACRGHGPPLVSVVCGSCGPGACRAGKAGVPP-GRQ 182
Db 184 VQDTGSAHCVCAAPCVSSPQGLGNNVNTLSSCHLQNTCFGRSIVHPGIC 43
Qy 184 VQDTGSAHCVCAAPCVSSPQGLGNNVNTLSSCHLQNTCFGRSIVHPGIC 43
Qy 184 VQDTGSAHCVCAAPCVSSPQGLGNNVNTLSSCHLQNTCFGRSIVHPGIC 43
Db 183 VQDTGSAHCVCAAPCVSSPQGLGNNVNTLSSCHLQNTCFGRSIVHPGIC 42
Qy 183 VQDTGSAHCVCAAPCVSSPQGLGNNVNTLSSCHLQNTCFGRSIVHPGIC 42
Qy 183 VQDTGSAHCVCAAPCVSSPQGLGNNVNTLSSCHLQNTCFGRSIVHPGIC 42
Db 244 AGTPEEPGESA 256
Qy 244 AGTPEEPGESA 256
Qy 244 AGTPEEPGESA 256
Qy 243 TQPTFKISGDA 255

RESULT 2 standard; Protein: 319 Aa.
AC 374600; Score 796; DB 1; Length 319;
Best Local Similarity 46.0%; Pred. No. 1,226-70; Matches 99; Conservative 46; Mismatches 67; Indels 3; Gaps 3;

Db 26 AVAGNMQSSKRGVLFVFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 85
Qy 26 AVAGNMQSSKRGVLFVFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 85
Qy 26 AVAGNMQSSKRGVLFVFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 85
Qy 30 SVYGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 88
Qy 30 SVYGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 88
Qy 30 SVYGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 88
Qy 86 PHCPKCKETGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 86 PHCPKCKETGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 86 PHCPKCKETGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 89 HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 147
Qy 89 HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 147
Qy 89 HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 147

Query Match 33.3% Score 796; DB 1; Length 319;
Best Local Similarity 46.0%; Pred. No. 1,226-70; Matches 99; Conservative 46; Mismatches 67; Indels 3; Gaps 3;

Db 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 83
Qy 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 83
Qy 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 83
Qy 28 EDSVPGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 86
Qy 28 EDSVPGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 86
Qy 28 EDSVPGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 86
Qy 84 GAKNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 143
Qy 84 GAKNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 143
Qy 84 GAKNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 143
Qy 87 VLV-HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 87 VLV-HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 87 VLV-HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 144 LLKAGKCHTGRGTSNTSTFVNSLTFPMHIFGCA 202
Qy 144 LLKAGKCHTGRGTSNTSTFVNSLTFPMHIFGCA 202
Qy 144 LLKAGKCHTGRGTSNTSTFVNSLTFPMHIFGCA 202
Qy 146 ELTAPKCHTGRGTSNTSTFVNSLTFPMHIFGCA 205
Qy 146 ELTAPKCHTGRGTSNTSTFVNSLTFPMHIFGCA 205
Qy 146 ELTAPKCHTGRGTSNTSTFVNSLTFPMHIFGCA 205

Query Match 33.3% Score 796; DB 1; Length 319;
Best Local Similarity 46.0%; Pred. No. 1,226-70; Matches 99; Conservative 46; Mismatches 67; Indels 3; Gaps 3;

Db 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 83
Qy 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 83
Qy 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 83
Qy 28 EDSVPGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 86
Qy 28 EDSVPGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 86
Qy 28 EDSVPGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 86
Qy 84 GAKNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 143
Qy 84 GAKNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 143
Qy 84 GAKNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 143
Qy 87 VLV-HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 87 VLV-HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 87 VLV-HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 144 LLKAGKCHTGRGTSNTSTFVNSLTFPMHIFGCA 202
Qy 144 LLKAGKCHTGRGTSNTSTFVNSLTFPMHIFGCA 202
Qy 144 LLKAGKCHTGRGTSNTSTFVNSLTFPMHIFGCA 202
Qy 146 ELTAPKCHTGRGTSNTSTFVNSLTFPMHIFGCA 205
Qy 146 ELTAPKCHTGRGTSNTSTFVNSLTFPMHIFGCA 205
Qy 146 ELTAPKCHTGRGTSNTSTFVNSLTFPMHIFGCA 205

Query Match 33.3% Score 796; DB 1; Length 319;
Best Local Similarity 46.0%; Pred. No. 1,226-70; Matches 99; Conservative 46; Mismatches 67; Indels 3; Gaps 3;

Db 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 83
Qy 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 83
Qy 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 83
Qy 28 EDSVPGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 86
Qy 28 EDSVPGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 86
Qy 28 EDSVPGVCGVAGSGATGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 86
Qy 84 GAKNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 143
Qy 84 GAKNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 143
Qy 84 GAKNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 143
Qy 87 VLV-HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 87 VLV-HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 87 VLV-HCLPCKSGVGVGQGGKATKSHKRCGASGNITFANSFTHPNT-SLIGLGLV 145
Qy 144 LLKAGKCHTGRGTSNTSTFVNSLTFPMHIFGCA 202
Qy 144 LLKAGKCHTGRGTSNTSTFVNSLTFPMHIFGCA 202
Qy 144 LLKAGKCHTGRGTSNTSTFVNSLTFPMHIFGCA 202
Qy 146 ELTAPKCHTGRGTSNTSTFVNSLTFPMHIFGCA 205
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Qy 146 ELTAPKCHTGRGTSNTSTFVNSLTFPMHIFGCA 205

Query Match 33.3% Score 796; DB 1; Length 319;
Best Local Similarity 46.0%; Pred. No. 1,226-70; Matches 99; Conservative 46; Mismatches 67; Indels 3; Gaps 3;

Db 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 83
Qy 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFVNSLTFPMHIFGCA 83
Qy 24 DRSKAGNTHVQAGKNGQVLTFLKSEKCHTGRGTSNTSTFV

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MPsrch_pp      protein - protein database search, using Smith-Waterman algorithm
Run on:        Wed Apr 12 07:46:37 2000:  MasPar time 36.61 Seconds
              640.186 Million cell updates/sec

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>US-09-276-268-16
Title:
Description:
(1-338), from US09276268 .pep
2401
Perfect Score:
Sequence: 1 MCAVNSALLVGGIGLAGALIL.....NRFLTGHEKDVVGGWGH 338
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No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	181	57.5	358	4	095210	2.14e-238
2	163	6.8	379	3	012596	1.28e-08
3	135	5.6	613	2	055222	1.37e-04
4	135	5.6	613	2	055222	1.37e-04
5	138	5.3	1149	5	000484	1.26e-03
6	128	5.3	491	5	081504	1.26e-03
7	124	5.5	295	10	020927	1.24e-03
8	125	5.2	538	3	020286	4.28e-03
9	123	5.1	502	5	016181	5.17e-03
10	123	5.1	902	5	016181	5.17e-03
11	122	5.1	1656	6	046392	5.74e-03
12	122	5.1	1453	11	063079	7.77e-03
13	122	5.1	1453	11	063079	7.77e-03
14	122	5.1	1460	6	095205	7.77e-03
15	122	5.0	160	6	095205	7.77e-03
16	120	5.0	290	5	093734	1.42e-02
17	119	5.0	290	5	044173	1.94e-02
18	119	5.0	347	6	094735	1.94e-02
19	119	5.0	347	6	094735	1.94e-02
20	120	5.0	692	2	030555	1.94e-02
21	120	5.0	692	2	030555	1.94e-02
22	120	5.0	853	2	053439	1.42e-02
23	120	5.0	853	2	053439	1.42e-02

21	121	5.0	890	5	07087	FIBRILLAR COLLAGEN C
22	121	5.0	1160	4	10406	COLZAI ALPRAI (11) COL
23	120	5.0	1364	6	06269	ALPRAI (11) COLLAGEN
24	120	5.0	1418	8	09519	ALPRAI (11) COLLAGEN
25	120	5.0	1418	8	09519	ALPRAI (11) COLLAGEN
26	120	5.0	1445	9	09321	ALPRAI 1 TYPE II COLLAG
27	121	5.0	1487	4	10407	ALPRAI 1 TYPE II COLLAG
28	119	5.0	1497	11	06431	PROCOLLAGEN TYPE V A
29	121	5.0	1531	10	09140	PROCOLLAGEN TYPE V A
30	121	5.0	1591	11	06380	HYPOCUTICULAR TYPE 8
31	120	5.0	1594	11	06380	TYPE VII COLLAGEN
32	121	5.0	1594	11	06380	TYPE VII COLLAGEN
33	121	5.0	1594	11	06380	TYPE VII COLLAGEN
34	121	5.0	1594	11	06380	TYPE VII COLLAGEN
35	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
36	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
37	119	4.9	639	3	01237	GLUCOMYLAASE PRECUR
38	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
39	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
40	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
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43	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
44	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
45	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
46	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
47	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
48	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
49	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
50	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
51	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
52	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
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54	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
55	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
56	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
57	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
58	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
59	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
60	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
61	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
62	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
63	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
64	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
65	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
66	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
67	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
68	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
69	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
70	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
71	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
72	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
73	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
74	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
75	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
76	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
77	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
78	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
79	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
80	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
81	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
82	117	4.9	639	3	01237	GLUCOMYLAASE PRECUR
83	117	4.9	639			

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT; 358 AA.
AC	095210; 1999	(TREMBLrel. 10. Created)	
MC	01-MAY-1999	(TREMBLrel. 10. Last sequence update)	
PC	01-MAY-1999	(TREMBLrel. 10. Last annotation update)	
DE	GENETHONIN 1.		
SE	Homo sapiens (Human)		
OS	Eukaryota; Metazoa; Chordata; Vertebrate; Mammalia;		
OC	Primates; Primates; Chordata; Homiidae; Homo.		
EN	(1)		
RP	SEQUENCE FROM N.A.		
AC	TISSUE-MUSCLE; 1996		
MC	01-MAY-1999		
PC	PIETU E., ALBERT O., GUICHARD V., LAMY B., BOIS F., LEROY E.,		
DE	MARTIG-SAMPSON R., HOULGADE R., SOULARIE P., AUFRAY C.:		
SE	"Novel gene transcripts preferentially expressed in human muscles		
OS	revealed by quantitative RT-PCR: identification of a high density cDNA array."		
OC	(2)		
EN	(1)		

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